

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo
- (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-162
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684
- (x) Note: In all the amino acid sequences below, "Xaa"
stands for one of the three stop codons.

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT	CGGCGTCGTA	CCAGCCGCTG	AAGCGGTTCT	CCAGGTTCCA	GGCGCTCTCG	60
CCATGCCGGA	TCAGCACCAG	CTTGTAGCTC	GTGCCGAATT	CGGCACGAGG	TTGCTTTGGG	120
AATGAGCAAG	GTCAAAACTG	CTCTGCACTC	ACAGACAACA	CTGAAGGGAA	GACACTGGCT	180
TCAGTAGTGA	AGGCTTCAGT	TTTTCGCCAG	CTAGGTGTAA	ACTGGGACAT	AGAGTGCTGG	240
ATGAAAGGGG	ACTTGACATT	ATTCATCTGT	CATATGGAGC	CATTACCTAA	GAACCCCTTC	300
AAGAATTATG	ACTCTAAGGT	CCATCTTTTA	TATGATCTGC	CTGAAGTCAT	AGATGATTCG	360
CCTCTGCCCC	CACTGAAAGA	CAGCTTTCAG	ACTGTCCAAT	GCAACTGCAG	TCTTCGGGGA	420
TGTGAATGTC	ATGTGCCGGT	ACCCAGAGCC	AAACTCAACT	ACGCTCTTCT	GATGTATTTG	480
GAAATCACAT	CTGCCGGTGT	GAGTTTTCAG	TCACCTCTGA	TGTCACTGCA	GCCCATGCTT	540
GTTGTGAAAC	CCGATCCACC	CTTAGGTTTG	CATATGGAAG	TCACAGATGA	TGGTAATTTA	600
AAGATTTCTT	GGGACAGCCA	AACAATGGCA	CCATTTCCGC	TTCAATATCA	GGTGAAATAT	660
TTAGAGAATT	CTACAATTGT	AAGAGAGGCT	GCTGAAATTG	TCTCAGCTAC	ATCTCTGCTG	720
GTAGACAGTG	TGCTTCCTGG	ATCTTCATAT	GAGGTCCAGG	TGAGGAGCAA	GAGACTGGAT	780
GGTTCAGGAG	TCTGGAGTGA	CTGGAGTTCA	CCTCAAGTCT	TTACCACACA	AGATGTTGTG	840
TATTTTCCAC	CCAAAATTCT	GACTAGTGTT	GGATCGAATG	CTTCTTTTCA	TTGCATCTAC	900
AAAAACGAAA	ACCAGATTAT	CTCCTCAAAA	CAGATAGTTT	GGTGGAGGAA	TCTAGCTGAG	960
AAAATCCCTG	AGATACAGTA	CAGCATTGTG	AGTGACCGAG	TTAGCAAAGT	TACCTTCTCC	1020
AACCTGAAAG	CCACCAGACC	TCGAGGGAAG	TTTACCTATG	ACGCAGTGTA	CTGCTGCAAT	1080
GAGCAGGCGT	GCCATCACCG	CTATGCTGAA	TTATACGTGA	TCGATGTCAA	TATCAATATA	1140
TCATGTGAAA	CTGACGGGTA	CTTAACATAA	ATGACTTGCA	GATGGTCACC	CAGCACAATC	1200
CAATCACTAG	TGGGAAGCAC	TGTGCAGCTG	AGGTATCACA	GGCGCAGCCT	GTATTGTCCT	1260
GATAGTCCAT	CTATTCATCC	TACGTCTGAG	CCCAAAACT	GCGTCTTACA	GAGAGACGGC	1320
TTTTATGAAT	GTGTTTTCCA	GCCAATCTTT	CTATTATCTG	GCTATACAAT	GTGGATCAGG	1380
ATCAACCATT	CTTTAGGTTC	ACTTGACTCG	CCACCAACGT	GTGTCCTTCC	TGACTCCGTA	1440
GTAAAACCAC	TACCTCCATC	TAACGTAAAA	GCAGAGATTA	CTGTAAACAC	TGGATTATTG	1500
AAAGTATCTT	GGGAAAAGCC	AGTCTTTCCG	GAGAATAACC	TTCAATTCCA	GATTCGATAT	1560
GGCTTAAGTG	GAAAAGAAAT	ACAATGGAAG	ACACATGAGG	TATTCGATGC	AAAGTCAAAG	1620
TCTGCCAGCC	TGCTGGTGTC	AGACCTCTGT	GCAGTCTATG	TGGTCCAGGT	TCGCTGCCGG	1680
CGGTTGGATG	GACTAGGATA	TTGGAGTAAT	TGGAGCAGTC	CAGCCTATAC	GCTTGTCATG	1740
GATGTAAAAG	TTCTATGAG	AGGGCCTGAA	TTTTGGAGAA	AAATGGATGG	GGACGTTACT	1800
AAAAAGGAGA	GAAATGTCAC	CTTGCTTTGG	AAGCCCCTGA	CGAAAAATGA	CTCACTGTGT	1860
AGTGTGAGGA	GGTACGTGGT	GAAGCATCGT	ACTGCCACAC	ATGGGACGTG	GTCAGAAGAT	1920

GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT 1980
 CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC 2040
 ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC 2100
 ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG 2160
 AAGATCCTTA ATGAAGATGA TGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG 2220
 TTTTATATCC ACGATAATTT TATTCCTATC GAGAAATATC AGTTTAGTCT TTACCCAGTA 2280
 TTTATGGAAG GAGTTGGAAG ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC 2340
 AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTT CTCTTGTGTC 2400
 CTACTGCTCG GAACACTGTT AATTTACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT 2460
 GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520
 ACTCTTTGA 2529

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly	Leu	Arg	Ser	Ala	Ser	Tyr	Gln	Pro	Leu	Lys	Arg	Phe	Ser	Arg	Phe
1				5					10					15	
Gln	Ala	Leu	Ser	Pro	Cys	Arg	Ile	Ser	Thr	Ser	Leu	Xaa	Leu	Val	Pro
			20					25					30		
Asn	Ser	Ala	Arg	Gly	Cys	Phe	Gly	Asn	Glu	Gln	Gly	Gln	Asn	Cys	Ser
		35					40					45			
Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	Ser	Val	Val	Lys
	50					55					60				
Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	Ile	Glu	Cys	Trp
65					70					75					80
Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	Glu	Pro	Leu	Pro
				85					90					95	
Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	Leu	Leu	Tyr	Asp
			100					105					110		

Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	Leu	Lys	Asp	Ser	115	120	125
Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	Cys	Glu	Cys	His	130	135	140
Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu	145	150	155
Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu	165	170	175
Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met	180	185	190
Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr	195	200	205
Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser	210	215	220
Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu	225	230	235
Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser	245	250	255
Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln	260	265	270
Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr	275	280	285
Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn	290	295	300
Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu	305	310	315
Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	Arg	Val	Ser	Lys	325	330	335
Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	Gly	Lys	Phe	Thr	340	345	350
Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	His	His	Arg	Tyr	355	360	365
Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	Ser	Cys	Glu	Thr	370	375	380
Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Pro	Ser	Thr	Ile	385	390	395
Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr	His	Arg	Arg	Ser	405	410	415
Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr	Ser	Glu	Pro	Lys	420	425	430
Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys	Val	Phe	Gln	Pro	435	440	445
Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg	Ile	Asn	His	Ser	450	455	460

Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu	Pro	Asp	Ser	Val	465	470	475	480
Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu	Ile	Thr	Val	Asn	485	490		495
Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val	Phe	Pro	Glu	Asn	500	505		510
Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly	Lys	Glu	Ile	Gln	515	520	525	
Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys	Ser	Ala	Ser	Leu	530	535	540	
Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln	Val	Arg	Cys	Arg	545	550	555	560
Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser	Ser	Pro	Ala	Tyr	565	570		575
Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly	Pro	Glu	Phe	Trp	580	585		590
Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg	Asn	Val	Thr	Leu	595	600	605	
Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	610	615	620	
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	625	630	635	640
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	645	650		655
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	660	665	670	
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	675	680	685	
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	690	695	700	
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	705	710	715	720
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	725	730		735
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	740	745	750	
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	755	760	765	
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	770	775	780	
Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	785	790	795	800
Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	805	810		815

Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
820 825 830

Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
835 840

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2848 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT	60
GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG	120
GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATTT TAGAATGGGA AGAATTAGGA	180
AGATGAATGG AGCCTGTGTC TTTCACTACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG	240
TCAGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAG	300
CCTGGGTTAC TTCTTATCAT CCTTAATTTT GAAAGCTAAG AGGGCCTAAC CATCAAGAAC	360
GTCCTGGAGG AAAGAATGTT TTTAACGCCA TTATTCAGTC AAAGAAATTA AGACTTGAGA	420
GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA	480
TGNGGCCCTA CCCACGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTTCTAACTC	540
AGAGACTCTT GTTCTAGTCT GTGNTATAAA ATTCAGCTTG TGGAAGCTTT CTGAGGGGTT	600
GGCAGCATTC AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGTT	660
ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC	720
TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCCC AGGGCCCCAA	780
AATAGCCGCT GTTATTTGTT AACCTTCAAG GTTTTCTGTT TGTTTATCTG TTTCTTGCGC	840
AGGATCATCT TCCAAGCACA TCCTGGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA	900
CTATGGTGAC ATCTGAGCTT CCTTGGTTCT TCACAGAACA TAAGCAGTTC CTTTGCTTGC	960
TTGTTAGATG AGAAAACTTC CTTGTCAGTC TGTCTCTACG ACTAGAATGG AAAGCCTTAC	1020
TACTTCCTAT GTATTCTTAA TATTTCAAAT GTCCTAATTA TGTTTGCTT CTCTGTCTTT	1080
AAGGGATTTA GTCTCTGGAT TTGAAGAAAT AAATAAATAA ATAAAGGAAA ACTAATTTTC	1140

TCGTGCCGGA	TGACTGCTAG	CTGAGCTCAG	GCCTACTGCA	TTCTACATTT	CGACTCTCTC	1200
CCTCTTCCCC	AGTGCTTTAG	CACTGGACTG	GGCAGTNCCT	GGCCTGGTCT	AACTCCTGTT	1260
TCCTGGTGGG	AATGTATAAT	AAGAACTCCA	TGAGTTCTGG	TATAAAACACT	GTGGTCTGTG	1320
TGCTAATTAA	ATCTNGTGTT	TCCTACAGCC	CCTGACGAAA	AATGACTCAC	TGTGTAGTGT	1380
GAGGAGGTAC	GTGGTGAAGC	ATCGTACTGC	CCACAATGGG	ACGTGGTCAG	AAGATGTGGG	1440
AAATCGGACC	AATCTCACTT	TCCTGTGGAC	AGAACCAGCG	CACACTGTTA	CAGTTCTGGC	1500
TGTCAATTCC	CTCGGCGCTT	CCCTTGTGAA	TTTTAACCTT	ACCTTCTCAT	GGCCCATGAG	1560
TAAAGTGAGT	GCTGTGGAGT	CACTCAGTGC	TTATCCCCTG	AGCAGCAGCT	GTGTCATCCT	1620
TTCTGGACA	CTGTCACCTG	ATGATTATAG	TCTGTTATAT	CTGGTTATTG	AATGGAAGAT	1680
CCTTAATGAA	GATGATGGAA	TGAAGTGGCT	TAGAATTCCC	TCGAATGTTA	AAAAGTTTTA	1740
TATCCACGAT	AATTTTATTC	CCATCGAGAA	ATATCAGTTT	AGTCTTTACC	CAGTATTTAT	1800
GGAAGGAGTT	GGAAAACCAA	AGATAATTAA	TGGTTTCACC	AAAGATGCTA	TCGACAAGCA	1860
GCAGAATGAC	GCAGGGCTGT	ATGTCATTGT	ACCCATAATT	ATTTCTCTCT	GTGTCCTACT	1920
GCTCGGAACA	CTGTTAATTT	CACACCAGAG	AATGAAAAAG	TTGTTTTGGG	ACGATGTTCC	1980
AAACCCCAAG	AATTGTTCTT	GGGCACAAGG	ACTGAATTTT	CAAAAGCCTG	AAACATTNGA	2040
GCATCTTTTT	ACCAAGCATG	CAGAATCAGT	GATATTTGGT	CCTCTTCTTC	TGGAGCCTGA	2100
ACCCATTTCA	GAAGAAATCA	GTGTCGATAC	AGCTTGGAAG	AATAAAGATG	AGATGGTCCC	2160
AGCAGCTATG	GTCTCCCTNC	TNNGGACCAC	ACCAGACCCT	GAAAGCAGTT	CTATTTGTNT	2220
TAGTGACCAG	TGTAACAGTG	CTAACTTCTC	TGGGTCTCAG	AGCACCCAGG	TAACCTGTGA	2280
GGATGAGTGT	CAGAGACAAC	CCTCAGTTAA	ATATGCAACT	CTGGTCAGCA	ACGATAAACT	2340
AGTGGAAGCT	GATGAAGAGC	AAGGGTTTAT	CCATAGTCCT	GTCAGCAACT	GCATCTCCAG	2400
TAATCATTCC	CCACTGAGGC	AGTCTTTCTC	TAGCAGCTCC	TGGGAGACAG	AGGCCAGAC	2460
ATTTTTCTCT	TTATCAGACC	AGCAACCCAC	CATGATTTCA	CCACAACCTT	CATTCTCGGG	2520
GTTGGATGAG	CTTTTGGAAC	TGGAGGGAAG	TTTTCTTGAA	GAAAATCACA	GGGAGNAGTC	2580
TGTCTGTTAT	CTAGGAGTCA	CCTCCGTCCN	CAGAAGAGAG	AGTGGTGTGC	TTTTGACTGG	2640
TGAGGCAGGA	ATCCTGTGCA	CATTCCCAGC	CCAGTGTCTG	TTCAGTGACA	TCAGGATCCT	2700
CCAGGAGAGA	TGCTCACACT	TTGTAGAAAA	TAATTTGAGT	TTAGGGACCT	CTGGTGAGAA	2760
CTTTGGTCCT	AACATGCCCC	AATTCCAAAC	CTGTTCCACG	CACAGTCACA	AGATAATGGA	2820
GAATAAGATG	TGTGACTTAA	CTGTGTAA				2848

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Ile	Lys	Glu	1	5	10	15
Asn	Phe	Ser	Arg	Ala	Gly	Leu	Leu	Ala	Glu	Leu	Arg	Pro	Thr	Ala	Phe	20	25	30	
Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala	Leu	Asp	Trp	35	40	45	
Ala	Val	Pro	Gly	Leu	Val	Leu	Leu	Phe	Pro	Gly	Gly	Asn	Val	Glu	Leu	50	55	60	
His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu	Cys	Ala	Asn	Ile	Xaa	Cys	65	70	75	80
Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	85	90	95	
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	100	105	110	
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	115	120	125	
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	130	135	140	
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	145	150	155	160
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	165	170	175	
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	180	185	190	
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	195	200	205	
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	210	215	220	
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	225	230	235	240
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	245	250	255	
Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	260	265	270	

Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu
		275					280					285			
Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly
	290					295					300				
Leu	Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His
305					310					315					320
Ala	Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile
				325					330					335	
Ser	Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met
			340					345					350		
Val	Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu
		355					360					365			
Ser	Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser
	370					375					380				
Gly	Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro
385					390					395					400
Ser	Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr
				405					410					415	
Asp	Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser
			420					425					430		
Ser	Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu
		435					440					445			
Thr	Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met
	450					455					460				
Ile	Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu
465					470					475					480
Glu	Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr
				485					490					495	
Leu	Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr
			500					505					510		
Gly	Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser
		515					520					525			
Asp	Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn
	530					535					540				
Leu	Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln
545					550					555					560
Phe	Gln	Thr	Cys	Ser	Thr	His	Ser	His	Lys	Ile	Met	Glu	Asn	Lys	Met
				565					570					575	
Cys	Asp	Phe	Thr	Val											
				580											

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 961 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTCGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTTCCTGGT GGGAAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT	540
CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720
TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTTCCT CTTGTGTCCT	840
ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA	960
A	961

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Xaa	Ile	Lys	1	5	10	15
Glu	Asn	Xaa	Phe	Ser	Arg	Ala	Gly	Xaa	Leu	Leu	Ala	Glu	Leu	Arg	Pro	20	25	30	
Thr	Ala	Phe	Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala	35	40	45	
Leu	Asp	Trp	Ala	Val	Pro	Gly	Leu	Val	Xaa	Leu	Leu	Phe	Pro	Gly	Gly	50	55	60	
Asn	Val	Xaa	Xaa	Glu	Leu	His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu	65	70	75	80
Cys	Ala	Asn	Xaa	Ile	Xaa	Cys	Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp	85	90	95	
Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	100	105	110	
Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	115	120	125	
Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	130	135	140	
Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	145	150	155	160
Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	165	170	175	
Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	180	185	190	
Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	195	200	205	
Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	210	215	220	
Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	225	230	235	240
Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	245	250	255	
Ala	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	260	265	270	
Ile	Ile	Ile	Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	275	280	285	
His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	290	295	300	
Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Val	Thr	Val					

305

310

315

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCCT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAAGTGTCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTCGCCTC TGCCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTTG TGAAACCCGA TCCACCCTTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTTGGGA CAGCCAAACA	780
ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960
AGTTCACCTC AAGTCTTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGAGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT	1260

GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAAGTGCCT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGAAA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTGAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTGCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTTAC	CCAGTATTTA	TGGAAGGAGT	TGGAACCA	2460
AAGATAATTA	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520
TATGTCATTG	TACCCATAAT	TATTTCTCT	TGTGTCCTAC	TGCTCGGAAC	ACTGTTAATT	2580
TCACACCAGA	GAATGAAAAA	GTTGTTTTGG	GACGATGTTT	CAAACCCCAA	GAATTGTTCC	2640
TGGGCACAAG	GACTGAATTT	CCAAAAGGAT	ATATCTTTAC	ATGAAGTTTT	TATTTTCAGA	2700
TAG						2703

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu	1	5	10	15
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys	20	25	30	
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu	35	40	45	
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser	50	55	60	
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro	65	70	75	80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly	85	90	95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	100	105	110	
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	115	120	125	
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	130	135	140	
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	145	150	155	160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	165	170	175	
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	180	185	190	
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	195	200	205	
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	210	215	220	
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	225	230	235	240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	245	250	255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	260	265	270	
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	275	280	285	
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	290	295	300	
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp				

305					310					315				320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro
				325					330					335
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile
			340					345					350	Tyr
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp
		355					360					365		Arg
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser
	370					375					380			Asp
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro
385					390					395				400
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala
				405					410					415
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn
			420					425					430	Ile
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp
		435					440					445		Ser
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg
	450					455					460			Tyr
His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro
465					470					475				480
Ser	Glu	Pro	Lys	Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu
				485					490					495
Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile
			500					505					510	Arg
Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val
	515						520					525		Leu
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala
	530					535					540			Glu
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro
545					550					555				560
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser
				565					570					575
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser
			580					585					590	Lys
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val
		595					600					605		Gln
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp
	610					615					620			Ser
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg
625					630					635				Gly
Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu
				645					650					655

Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	660	665	670
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	675	680	685
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	690	695	700
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	705	710	715
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	725	730	735
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	740	745	750
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	755	760	765
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	770	775	780
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	785	790	795
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	805	810	815
Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	820	825	830
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	835	840	845
Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	850	855	860
Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	865	870	875
Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Asp	Ile	Ser	Leu	His	Glu	Val	885	890	895
Phe	Ile	Phe	Arg													900		

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGAATCGT	TCTGCAAATC	CAGGTGTACA	CCTCTGAAGA	AAGATGATGT	GTCAGAAATT	60
CTATGTGGTT	TTGTTACACT	GGGAATTTCT	TTATGTGATA	GCTGCACTTA	ACCTGGCATA	120
TCCAATCTCT	CCCTGGAAAT	TTAAGTTGTT	TTGTGGACCA	CCGAACACAA	CCGATGACTC	180
CTTTCTCTCA	CCTGCTGGAG	CCCCAAACAA	TGCCTCGGCT	TTGAAGGGGG	CTTCTGAAGC	240
AATTGTTGAA	GCTAAATTTA	ATTCAAGTGG	TATCTACGTT	CCTGAGTTAT	CCAAAACAGT	300
CTTCCACTGT	TGCTTTGGGA	ATGAGCAAGG	TCAAACTGTC	TCTGCACTCA	CAGACAACAC	360
TGAAGGGAAG	ACACTGGCTT	CAGTAGTGAA	GGCTTCAGTT	TTTCGCCAGC	TAGGTGTAAA	420
CTGGGACATA	GAGTGCTGGA	TGAAAGGGGA	CTTGACATTA	TTCATCTGTC	ATATGGAGCC	480
ATTACCTAAG	AACCCCTTCA	AGAATTATGA	CTCTAAGGTC	CATCTTTTAT	ATGATCTGCC	540
TGAAGTCATA	GATGATTCGC	CTCTGCCCCC	ACTGAAAGAC	AGCTTTTCAGA	CTGTCCAATG	600
CAACTGCAGT	CTTCGGGGAT	GTGAATGTCA	TGTGCCGGTA	CCCAGAGCCA	AACTCAACTA	660
CGCTCTTCTG	ATGTATTTGG	AAATCACATC	TGCCGGTGTG	AGTTTTCAGT	CACCTCTGAT	720
GTCAGTGCAG	CCCATGCTTG	TTGTGAAACC	CGATCCACCC	TTAGGTTTGC	ATATGGAAGT	780
CACAGATGAT	GGTAATTTAA	AGATTTCTTG	GGACAGCCAA	ACAATGGCAC	CATTTCCGCT	840
TCAATATCAG	GTGAAATATT	TAGAGAATTC	TACAATTGTA	AGAGAGGCTG	CTGAAATTGT	900
CTCAGCTACA	TCTCTGCTGG	TAGACAGTGT	GCTTCCTGGA	TCTTCATATG	AGGTCCAGGT	960
GAGGAGCAAG	AGACTGGATG	GTTCAGGAGT	CTGGAGTGAC	TGGAGTTCAC	CTCAAGTCTT	1020
TACCACACAA	GATGTTGTGT	ATTTTCCACC	CAAAATTCTG	ACTAGTGTTG	GATCGAATGC	1080
TTCTTTTCAT	TGCATCTACA	AAAACGAAAA	CCAGATTATC	TCCTCAAAAC	AGATAGTTTG	1140
GTGGAGGAAT	CTAGCTGAGA	AAATCCCTGA	GATACAGTAC	AGCATTGTGA	GTGACCGAGT	1200
TAGCAAAGTT	ACCTTCTCCA	ACCTGAAAGC	CACCAGACCT	CGAGGGAAGT	TTACCTATGA	1260
CGCAGTGTAC	TGCTGCAATG	AGCAGGCGTG	CCATCACCGC	TATGCTGAAT	TATACGTGAT	1320
CGATGTCAAT	ATCAATATAT	CATGTGAAAC	TGACGGGTAC	TTAACTAAAA	TGACTTGCAG	1380
ATGGTCACCC	AGCACAATCC	AATCACTAGT	GGGAAGCACT	GTGCAGCTGA	GGTATCACAG	1440
GCGCAGCCTG	TATTGTCCTG	ATAGTCCATC	TATTCATCCT	ACGTCTGAGC	CCAAAACTG	1500
CGTCTTACAG	AGAGACGGCT	TTTATGAATG	TGTTTTCCAG	CCAATCTTTC	TATTATCTGG	1560
CTATACAATG	TGGATCAGGA	TCAACCATTG	TTTAGGTTCA	CTTGACTCGC	CACCAACGTG	1620
TGTCCTTCCT	GACTCCGTAG	TAAAACCACT	ACCTCCATCT	AACGTAAAAG	CAGAGATTAC	1680
TGTAAACACT	GGATTATTGA	AAGTATCTTG	GGAAAAGCCA	GTCTTCCGG	AGAATAACCT	1740
TCAATTCCAG	ATTCGATATG	GCTTAAGTGG	AAAAGAAATA	CAATGGAAGA	CACATGAGGT	1800
ATTCGATGCA	AAGTCAAAGT	CTGCCAGCCT	GCTGGTGTCA	GACCTCTGTG	CAGTCTATGT	1860

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GGTCCAGGTT CGCTGCCGGC GGTGGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC      1920
AGCCTATACG CTTGTCATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA      1980
AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTTGGA AGCCCCTGAC      2040
GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCCACAA      2100
TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCCTGT GGACAGAACC      2160
AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTTAA      2220
CCTTACCTTC TCATGGCCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC      2280
CCTGAGCAGC AGCTGTGTCA TCCTTTCCTG GAACTGTGCA CCTGATGATT ATAGTCTGTT      2340
ATATCTGGTT ATTGAATGGA AGATCCTTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT      2400
TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA      2460
G                                                                 2461

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1              5              10              15
Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20              25              30
Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35              40              45
Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50              55              60
Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65              70              75
Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85              90              95
Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100             105             110

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Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp		
		115					120					125					
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met		
	130					135					140						
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His		
145					150					155					160		
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro		
				165					170					175			
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly		
			180					185					190				
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu		
		195					200					205					
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro		
	210					215					220						
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu		
225					230					235					240		
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp		
				245					250					255			
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr		
			260					265					270				
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala		
		275					280					285					
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val		
	290					295					300						
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp		
305					310					315					320		
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro		
			325						330					335			
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr		
			340					345					350				
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg		
		355					360					365					
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp		
	370					375					380						
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg		
385					390					395					400		
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys		
			405						410					415			
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile		
			420					425					430				
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser		
		435					440					445					
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr		
	450					455					460						

[illegible]

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn	Phe	Gln	Lys	Arg	Thr	Asp	Leu
1				5			

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rb
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala
1			5					10						15	
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser
		20					25					30			
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val
		35				40						45			
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser
	50					55					60				
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly
65					70				75						80

Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro Ser
 85 90 95
 Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr Asp
 100 105 110
 Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser Ser
 115 120 125
 Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Ser Trp Glu Thr
 130 135 140
 Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Glu Gln Pro Thr Met Ile
 145 150 155 160
 Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu
 165 170 175
 Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu
 180 185 190
 Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly
 195 200 205
 Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp
 210 215 220
 Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu
 225 230 235 240
 Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln Phe
 245 250 255
 Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys
 260 265 270
 Asp Phe Thr Val
 275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val
 1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rd
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn	Phe	Gln	Lys	Asp	Ile	Ser	His	Glu	Val	Phe	Ile	Phe	Arg
1				5					10				

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Re
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Tyr	Ile	His	Gly	Met	Cys	Thr	Val	Leu	Phe	Met	Asp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
1				5					10					15	
Ser	Glu	Pro	Lys												
				20											

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn
1				5					10					15	
Cys Ser Trp															

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG	CCGAGGGAAT	TGACAGCCAG	AACTGTAACA	GTGTGCGCTG	GTTCTGTCCA	60
CAGGAAAGTG	AGATTGGTCC	GATTTCCCAC	ATCTTCTGAC	CACGTCCCAT	TGTGGGCAGT	120
ACGATGCTTC	ACCACGTACC	TCCTCACACT	ACACAGTGAG	TCATTT		166

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCT	120
CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG GTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTTCATT TGATGTTCAG      60
AAGTCAGCAA GGTTCCTCATA TGTCCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG      120
CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT      180
TAAAGATACG AG                                                                192

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(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

AGACTGACAA GGAAGTTTTTC TCATCTAACA AGCAAGCAAA GGAAGTCTT ATGTNCTGTG      60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT      120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA
168

```

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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AGAATTATGA CTCTAAGGTC CATGTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC      60

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CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTGG	180
NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCAGTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACTTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTCAG	240
AACGATTCT	250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC	18
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(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTTCGTACCC GACGTCACTG

20